



SEQUENCE LISTING

<110> Piddington, Christopher S.
 Petrie, Charles
 Shoemaker, Kimberly E.
 Bishop, Paul D.

<120> ZACE2: A HUMAN METALLOENZYME

<130> 99-24C1

<150> 60/133.952

<151> 1999-05-13

<150> 60/151.181

<151> 1999-08-27

<150> 09/563.516

<151> 2000-05-03

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<170> FastSEQ for Windows Version 3.0

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<213> Homo sapiens

<220>

<221> CDS

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Leu Leu Ser Leu Val Ala Val Thr Ala Ala Gln Ser Thr Ile Glu Glu	
10 15 20	

09978385-101601

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ttc tat caa agt tca ctt gct tct tgg aat tat aac acc aat att act Phe Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr Asn Ile Thr 40 45 50 55	199
gaa gag aat gtc caa aac atg aat aat gct ggg gac aaa tgg tct gcc Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly Asp Lys Trp Ser Ala 60 65 70	247
ttt tta aag gaa cag tcc aca ctt gcc caa atg tat cca cta caa gaa Phe Leu Lys Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro Leu Gln Glu 75 80 85	295
att cag aat ctc aca gtc aag ctt cag ctg cag gct ctt cag caa aat Ile Gln Asn Leu Thr Val Lys Leu Gln Leu Gln Ala Leu Gln Gln Asn 90 95 100	343
ggg tct tca gtg ctc tca gaa gac aag agc aaa cgg ttg aac aca att Gly Ser Ser Val Leu Ser Glu Asp Lys Ser Lys Arg Leu Asn Thr Ile 105 110 115	391
cta aat aca atg agc acc atc tac agt act gga aaa gtt tgt aac cca Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val Cys Asn Pro 120 125 130 135	439
gat aat cca caa gaa tgc tta tta ctt gaa cca ggt ttg aat gaa ata Asp Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu Asn Glu Ile 140 145 150	487
atg gca aac agt tta gac tac aat gag agg ctc tgg gct tgg gaa agc Met Ala Asn Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala Trp Glu Ser 155 160 165	535
tgg aga tct gag gtc ggc aag cag ctg agg cca tta tat gaa gag tat Trp Arg Ser Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr Glu Glu Tyr 170 175 180	583
gtg gtc ttg aaa aat gag atg gca aga gca aat cat tat gag gac tat Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn His Tyr Glu Asp Tyr 185 190 195	631

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Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Val Asn Gly Val Asp Gly Tyr	
200 205 210 215	
gac tac agc cgc ggc cag ttg att gaa gat gtg gaa cat acc ttt gaa	727
Asp Tyr Ser Arg Gly Gln Leu Ile Glu Asp Val Glu His Thr Phe Glu	
220 225 230	
gag att aaa cca tta tat gaa cat ctt cat gcc tat gtg agg gca aag	775
Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val Arg Ala Lys	
235 240 245	
ttg atg aat gcc tat cct tcc tat atc agt cca att gga tgc ctc cct	823
Leu Met Asn Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly Cys Leu Pro	
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gct cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca aat ctg tac	871
Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr Asn Leu Tyr	
265 270 275	
tct ttg aca gtt ccc ttt gga cag aaa cca aac ata gat gtt act gat	919
Ser Leu Thr Val Pro Phe Gly Gln Lys Pro Asn Ile Asp Val Thr Asp	
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Ala Met Val Asp Gln Ala Trp Asp Ala Gln Arg Ile Phe Lys Glu Ala	
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Glu Lys Phe Phe Val Ser Val Gly Leu Pro Asn Met Thr Gln Gly Phe	
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Trp Glu Asn Ser Met Leu Thr Asp Pro Gly Asn Val Gln Lys Ala Val	
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Cys His Pro Thr Ala Trp Asp Leu Gly Lys Gly Asp Phe Arg Ile Leu	
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 cta aga aat gga gct aat gaa gga ttc cat gaa gct gtt ggg gaa atc 1255
 Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile
 395 400 405
 atg tca ctt tct gca gcc aca cct aag cat tta aaa tcc att ggt ctt 1303
 Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu
 410 415 420
 ctg tca ccc gat ttt caa gaa gac aat gaa aca gaa ata aac ttc ctg 1351
 Leu Ser Pro Asp Phe Gln Glu Asp Asn Glu Thr Glu Ile Asn Phe Leu
 425 430 435
 ctc aaa caa gca ctc acg att gtt ggg act ctg cca ttt act tac atg 1399
 Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe Thr Tyr Met
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 cag tgg atg aaa aag tgg tgg gag atg aag cga gag ata gtt ggg gtg 1495
 Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val
 475 480 485
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 Val Glu Pro Val Pro His Asp Glu Thr Tyr Cys Asp Pro Ala Ser Leu
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 Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr Thr Arg Thr
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097335-101601

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Gln Lys Leu Phe Asn Met Leu Arg Leu Gly Lys Ser Glu Pro Trp Thr	
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cta gca ttg gaa aat gtt gta gga gca aag aac atg aat gta agg cca	1783
Leu Ala Leu Glu Asn Val Val Gly Ala Lys Asn Met Asn Val Arg Pro	
570 575 580	
ctg ctc aac tac ttt gag ccc tta ttt acc tgg ctg aaa gac cag aac	1831
Leu Leu Asn Tyr Phe Glu Pro Leu Phe Thr Trp Leu Lys Asp Gln Asn	
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Lys Asn Ser Phe Val Gly Trp Ser Thr Asp Trp Ser Pro Tyr Ala Asp	
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caa agc atc aaa gtg agg ata agc cta aaa tca gct ctt gga gat aaa	1927
Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu Gly Asp Lys	
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gca tat gaa tgg aac gac aat gaa atg tac ctg ttc cga tca tct gtt	1975
Ala Tyr Glu Trp Asn Asp Asn Glu Met Tyr Leu Phe Arg Ser Ser Val	
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Ala Tyr Ala Met Arg Gln Tyr Phe Leu Lys Val Lys Asn Gln Met Ile	
650 655 660	
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Ser Phe Asn Phe Phe Val Thr Ala Pro Lys Asn Val Ser Asp Ile Ile	
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09978385-101601

Pro Arg Thr Glu Val Glu Lys Ala Ile Arg Met Ser Arg Ser Arg Ile
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aat gat gct ttc cgt ctg aat gac aac agc cta gag ttt ctg ggg ata 2215
Asn Asp Ala Phe Arg Leu Asn Asp Asn Ser Leu Glu Phe Leu Gly Ile
715 720 725

cag cca aca ctt gga cct cct aac cag ccc cct gtt tcc ata tgg ctg 2263
Gln Pro Thr Leu Gly Pro Pro Asn Gln Pro Pro Val Ser Ile Trp Leu
730 735 740

att gtt ttt gga gtt gtg atg gga gtg ata gtg gtt ggc att gtc atc 2311
Ile Val Phe Gly Val Val Met Gly Val Ile Val Val Gly Ile Val Ile
745 750 755

ctg atc ttc act ggg atc aga gat cgg aag aag aaa aat aaa gca aga 2359
Leu Ile Phe Thr Gly Ile Arg Asp Arg Lys Lys Lys Asn Lys Ala Arg
760 765 770 775

agt gga gaa aat cct tat gcc tcc atc gat att agc aaa gga gaa aat 2407
Ser Gly Glu Asn Pro Tyr Ala Ser Ile Asp Ile Ser Lys Gly Glu Asn
780 785 790

aat cca gga ttc caa aac act gat gat gtt cag acc tcc ttt 2449
Asn Pro Gly Phe Gln Asn Thr Asp Asp Val Gln Thr Ser Phe
795 800 805

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0978385-101501

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 <212> PRT
 <213> Homo sapiens

<400> 2

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			20					25					30		
Asn	His	Glu	Ala	Glu	Asp	Leu	Phe	Tyr	Gln	Ser	Ser	Leu	Ala	Ser	Trp
		35				40						45			
Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Val	Gln	Asn	Met	Asn	Asn
	50				55					60					
Ala	Gly	Asp	Lys	Trp	Ser	Ala	Phe	Leu	Lys	Glu	Gln	Ser	Thr	Leu	Ala
65				70					75					80	
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Thr	Gly	Lys	Val	Cys	Asn	Pro	Asp	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu
	130					135					140				
Glu	Pro	Gly	Leu	Asn	Glu	Ile	Met	Ala	Asn	Ser	Leu	Asp	Tyr	Asn	Glu
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Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg
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Ala	Asn	His	Tyr	Glu	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu
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Val	Asn	Gly	Val	Asp	Gly	Tyr	Asp	Tyr	Ser	Arg	Gly	Gln	Leu	Ile	Glu
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His	Ala	Tyr	Val	Arg	Ala	Lys	Leu	Met	Asn	Ala	Tyr	Pro	Ser	Tyr	Ile
			245						250					255	
Ser	Pro	Ile	Gly	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly
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Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Ser	Leu	Thr	Val	Pro	Phe	Gly	Gln	Lys
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09978385.101601

Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala
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 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
 305 310 315 320
 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
 325 330 335
 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
 340 345 350
 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
 355 360 365
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
 370 375 380
 Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
 385 390 395 400
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
 405 410 415
 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn
 420 425 430
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
 435 440 445
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
 450 455 460
 Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met
 465 470 475 480
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
 500 505 510
 Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala
 515 520 525
 Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile
 530 535 540
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu
 545 550 555 560
 Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala
 565 570 575
 Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe
 580 585 590
 Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr
 595 600 605
 Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
 610 615 620

09978385-101601

Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met
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 Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu
 645 650 655
 Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val
 660 665 670
 Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro
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 Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
 690 695 700
 Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
 705 710 715 720
 Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln
 725 730 735
 Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
 740 745 750
 Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
 755 760 765
 Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile
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 Val Gln Thr Ser Phe
 805

<210> 3
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 <212> DNA
 <213> Artificial Sequence

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 <223> n = A,T,C or G

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taycarwsnw snytngcnws ntggaaytay aayacnaaya thacngarga raaygtncar	180
aayatgaaya aygcnggnga yaartggwsn gcnttyytna argarcarsw nacnytngcn	240

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carcaraayg	gnwsnwsngt	nytnwsngar	gayaarwsna	armgnytnaa	yacnathytn	360
aayacnatgw	snacnathta	ywsnacnggn	aargtntgya	ayccngayaa	yccncargar	420
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caratgathy	tnnttyggnga	rgargaygt	mgngtngcna	ayytnaarcc	nmgnathwsn	2040
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<213> Artificial Sequence

097335-101501

<220>

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<210> 5

<211> 2638

<212> DNA

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<222> (106)...(2520)

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 Met Ser Ser Ser
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tcc tgg ctc ctt ctc agc ctt gtt gct gtt act act gct cag tcc ctc 165
 Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr Ala Gln Ser Leu
 5 10 15 20

acc gag gaa aat gcc aag aca ttt tta aac aac ttt aat cag gaa gct 213
 Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe Asn Gln Glu Ala
 25 30 35

gaa gac ctg tct tat caa agt tca ctt gct tct tgg aat tat aat act 261
 Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr
 40 45 50

aac att act gaa gaa aat gcc caa aag atg agt gag gct gca gcc aaa 309
 Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu Ala Ala Ala Lys
 55 60 65

tgg tct gcc ttt tat gaa gaa cag tct aag act gcc caa agt ttc tca 357
 Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala Gln Ser Phe Ser
 70 75 80

cta caa gaa atc cag act ccg atc atc aag cgt caa cta cag gcc ctt 405

09978385-101601

Leu	Gln	Glu	Ile	Gln	Thr	Pro	Ile	Ile	Lys	Arg	Gln	Leu	Gln	Ala	Leu	
85					90					95					100	
cag	caa	agt	ggg	tct	tca	gca	ctc	tca	gca	gac	aag	aac	aaa	cag	ttg	453
Gln	Gln	Ser	Gly	Ser	Ser	Ala	Leu	Ser	Ala	Asp	Lys	Asn	Lys	Gln	Leu	
			105						110					115		
aac	aca	att	ctg	aac	acc	atg	agc	acc	att	tac	agt	act	gga	aaa	gtt	501
Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser	Thr	Gly	Lys	Val	
			120						125				130			
tgc	aac	cca	aag	aac	cca	caa	gaa	tgc	tta	tta	ctt	gag	cca	gga	ttg	549
Cys	Asn	Pro	Lys	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu	Glu	Pro	Gly	Leu	
		135					140					145				
gat	gaa	ata	atg	gcg	aca	agc	aca	gac	tac	aac	tct	agg	ctc	tgg	gca	597
Asp	Glu	Ile	Met	Ala	Thr	Ser	Thr	Asp	Tyr	Asn	Ser	Arg	Leu	Trp	Ala	
	150					155					160					
tgg	gag	ggc	tgg	agg	gct	gag	gtt	ggc	aag	cag	ctg	agg	ccg	ttg	tat	645
Trp	Glu	Gly	Trp	Arg	Ala	Glu	Val	Gly	Lys	Gln	Leu	Arg	Pro	Leu	Tyr	
165					170					175					180	
gaa	gag	tat	gtg	gtc	ctg	aaa	aac	gag	atg	gca	aga	gca	aac	aat	tat	693
Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg	Ala	Asn	Asn	Tyr	
			185						190					195		
aac	gac	tat	ggg	gat	tat	tgg	aga	ggg	gac	tat	gaa	gca	gag	gga	gca	741
Asn	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu	Ala	Glu	Gly	Ala	
			200					205					210			
gat	ggc	tac	aac	tat	aac	cgt	aac	cag	ttg	att	gaa	gat	gta	gaa	cgt	789
Asp	Gly	Tyr	Asn	Tyr	Asn	Arg	Asn	Gln	Leu	Ile	Glu	Asp	Val	Glu	Arg	
		215					220					225				
acc	ttc	gca	gag	atc	aag	cca	ttg	tat	gag	cat	ctt	cat	gcc	tat	gtg	837
Thr	Phe	Ala	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu	His	Ala	Tyr	Val	
	230					235					240					
agg	agg	aag	ttg	atg	gat	acc	tac	cct	tcc	tac	atc	agc	ccc	act	gga	885
Arg	Arg	Lys	Leu	Met	Asp	Thr	Tyr	Pro	Ser	Tyr	Ile	Ser	Pro	Thr	Gly	
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tgc ctc cct gcc cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca 933
 Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr
 265 270 275

aat ctg tac cct ttg act gtt ccc ttt gca cag aaa cca aac ata gat 981
 Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys Pro Asn Ile Asp
 280 285 290

gtt act gat gca atg atg aat cag ggc tgg gat gca gaa agg ata ttt 1029
 Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala Glu Arg Ile Phe
 295 300 305

caa gag gca gag aaa ttc ttt gtt tct gtt ggc ctt cct cat atg act 1077
 Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu Pro His Met Thr
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caa gga ttc tgg gca aac tct atg ctg act gag cca gca gat ggc cgg 1125
 Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro Ala Asp Gly Arg
 325 330 335 340

aaa gtt gtc tgc cac ccc aca gct tgg gat ctg gga cac gga gac ttc 1173
 Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly His Gly Asp Phe
 345 350 355

aga atc aag atg tgt aca aag gtc aca atg gac aac ttc ttg aca gcc 1221
 Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn Phe Leu Thr Ala
 360 365 370

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 His His Glu Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Arg Gln
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cct ttc ctg cta aga aac gga gcc aat gaa ggg ttc cat gaa gct gtt 1317
 Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val
 390 395 400

gga gaa atc atg tca ctt tct gca gct acc ccc aag cat ctg aaa tcc 1365
 Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser
 405 410 415 420

att ggt ctt ctg cca tcc gat ttt caa gaa gat agc gaa aca gag ata 1413
 Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser Glu Thr Glu Ile
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09978385-101604

aac ttc cta ctg aaa cag gca ttg aca att gtt gga aca cta ccg ttt 1461
 Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe
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act tac atg tta gag aag tgg agg tgg atg gtc ttt cgg ggt gaa att 1509
 Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe Arg Gly Glu Ile
 455 460 465

ccc aaa gag cag tgg atg aaa aag tgg tgg gag atg aag cgg gag atc 1557
 Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile
 470 475 480

gtt ggt gtg gtg gag cct ctg cct cat gat gaa aca tac tgt gac cct 1605
 Val Gly Val Val Glu Pro Leu Pro His Asp Glu Thr Tyr Cys Asp Pro
 485 490 495 500

gca tct ctg ttc cat gtt tct aat gat tac tca ttc att cga tat tac 1653
 Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr
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aca agg acc att tac caa ttc cag ttt caa gaa gct ctt tgt caa gca 1701
 Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala
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 Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile Ser Asn Ser Thr
 535 540 545

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 Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu Gly Asn Ser Glu
 550 555 560

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 Pro Trp Thr Lys Ala Leu Glu Asn Val Val Gly Ala Arg Asn Met Asp
 565 570 575 580

gta aaa cca ctg ctc aat tac ttc caa ccg ttg ttt gac tgg ctg aaa 1893
 Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe Asp Trp Leu Lys
 585 590 595

gag cag aac aga aat tct ttt gtg ggg tgg aac act gaa tgg agc cca 1941

09978385-101604

Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr Glu Trp Ser Pro	
600 605 610	
tat gcc gac caa agc att aaa gtg agg ata agc cta aaa tca gct ctt	1989
Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu	
615 620 625	
gga gct aat gca tat gaa tgg acc aac aac gaa atg ttc ctg ttc cga	2037
Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met Phe Leu Phe Arg	
630 635 640	
tca tct gtt gca tat gcc atg aga aag tat ttt tca ata atc aaa aac	2085
Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Phe Ser Ile Ile Lys Asn	
645 650 655 660	
cag aca gtt cct ttt cta gag gaa gat gta cga gtg agc gat ttg aaa	2133
Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val Ser Asp Leu Lys	
665 670 675	
cca aga gtc tcc ttc tac ttc ttt gtc acc tca ccc caa aat gtg tct	2181
Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro Gln Asn Val Ser	
680 685 690	
gat gtc att cct aga agt gaa gtt gaa gat gcc atc agg atg tct cgg	2229
Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile Arg Met Ser Arg	
695 700 705	
ggc cgc atc aat gat gtc ttt ggc ctg aat gat aac agc ctg gag ttt	2277
Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn Ser Leu Glu Phe	
710 715 720	
ctg ggg att cac cca aca ctt gag cca cct tac cag cct cct gtc acc	2325
Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln Pro Pro Val Thr	
725 730 735 740	
ata tgg ctg att att ttt ggt gtt gtg atg gca ctg gta gtg gtt ggc	2373
Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu Val Val Val Gly	
745 750 755	
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092335-101604

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 Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met Asp Ile Gly Lys
 775 780 785

gga gaa agc aat gca gga ttc caa aac agt gat gat gct cag act tcc 2517
 Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp Ala Gln Thr Ser
 790 795 800

ttt tagcaaagca cttgtcatct tcctgtatgt aaatgctaac ttcatagtac 2570
 Phe
 805

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 gttgtcca 2638

<210> 6

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<400> 6

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 Asn Gln Glu Ala Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp
 35 40 45
 Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu
 50 55 60
 Ala Ala Ala Lys Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala
 65 70 75 80
 Gln Ser Phe Ser Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln
 85 90 95
 Leu Gln Ala Leu Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys
 100 105 110
 Asn Lys Gln Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser
 115 120 125

05978385-101601

Thr Gly Lys Val Cys Asn Pro Lys Asn Pro Gln Glu Cys Leu Leu Leu
 130 135 140
 Glu Pro Gly Leu Asp Glu Ile Met Ala Thr Ser Thr Asp Tyr Asn Ser
 145 150 155 160
 Arg Leu Trp Ala Trp Glu Gly Trp Arg Ala Glu Val Gly Lys Gln Leu
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 Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
 180 185 190
 Ala Asn Asn Tyr Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
 195 200 205
 Ala Glu Gly Ala Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu
 210 215 220
 Asp Val Glu Arg Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu
 225 230 235 240
 His Ala Tyr Val Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile
 245 250 255
 Ser Pro Thr Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
 260 265 270
 Arg Phe Trp Thr Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys
 275 280 285
 Pro Asn Ile Asp Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala
 290 295 300
 Glu Arg Ile Phe Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
 305 310 315 320
 Pro His Met Thr Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro
 325 330 335
 Ala Asp Gly Arg Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly
 340 345 350
 His Gly Asp Phe Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn
 355 360 365
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
 370 375 380
 Tyr Ala Arg Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
 385 390 395 400
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
 405 410 415
 His Leu Lys Ser Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser
 420 425 430
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
 435 440 445
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
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09070305.101601

Arg Gly Glu Ile Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met
 465 470 475 480
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Leu Pro His Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
 500 505 510
 Ile Arg Tyr Tyr Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala
 515 520 525
 Leu Cys Gln Ala Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile
 530 535 540
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu
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 Gly Asn Ser Glu Pro Trp Thr Lys Ala Leu Glu Asn Val Val Gly Ala
 565 570 575
 Arg Asn Met Asp Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe
 580 585 590
 Asp Trp Leu Lys Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr
 595 600 605
 Glu Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
 610 615 620
 Lys Ser Ala Leu Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met
 625 630 635 640
 Phe Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Phe Ser
 645 650 655
 Ile Ile Lys Asn Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val
 660 665 670
 Ser Asp Leu Lys Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro
 675 680 685
 Gln Asn Val Ser Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile
 690 695 700
 Arg Met Ser Arg Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn
 705 710 715 720
 Ser Leu Glu Phe Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln
 725 730 735
 Pro Pro Val Thr Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu
 740 745 750
 Val Val Val Gly Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg
 755 760 765
 Lys Lys Lys Asn Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met
 770 775 780
 Asp Ile Gly Lys Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp
 785 790 795 800

00978385-101601

Ala Gln Thr Ser Phe
805

<210> 7
<211> 2415
<212> DNA
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sequence of SEQ ID NO:6.

<221> misc_feature
<222> (1)...(2415)
<223> n = A,T,C or G

<400> 7

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taycarwsnw	snytngcnws	ntggaaytay	aayacnaaya	thacngarga	raaygcncar	180
aatatgwsng	argcngcngc	naartggwsn	gcnttytayg	argarcarws	naaracngcn	240
carwsnttyw	snytncarga	rathcaracn	ccnathatha	armgncaryt	ncargcnytn	300
carcarwsng	gnwsnwsngc	nytnwsngcn	gayaaraaya	arcarytnaa	yacnathytn	360
aayacnatgw	snacnathta	ywsnacnggn	aargtntgya	ayccnaaraa	yccncargar	420
tgyytntytny	tngarccngg	nytngaygar	athatggcna	cnwsnacnga	ytayaaywsn	480
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gargartayg	tngtnytnaa	raaygaratg	gcnmgngcna	ayaaytayaa	ygaytayggg	600
gaytaytgmm	gngngayta	ygargcngar	gngcngayg	gntayaayta	yaaymgnaay	660
carytnathg	argaygtnga	rmgnacntty	gcngaratha	arccnytnnta	ygarcayytn	720
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aargtngtnt	gyayccnac	ngcntgggag	ytnggncayg	gngaytymg	nathaaratg	1080
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caygargcng	tngngarat	hatgwsnytn	wsngcngcna	cncnaarca	yytnaarwsn	1260
athggnytny	tnccnwsnga	ytytcargar	gaywsngara	cngarathaa	ytyytnytn	1320
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09978385 "101601"

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 mgnathwsny tnaarwsngc nytnngngcn aaygcntayg artggacnaa yaaygaratg 1920
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 caracngtn cnttytnga rgargaygn mgngtnwsng ayytnaarcc nmngntnwsn 2040
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<220>

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 Met Ser Ser Ser
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tcc tgg ctc ctt ctc agc ctt gtt gct gtt act act gct cag tcc ctc 165
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acc gag gaa aat gcc aag aca ttt tta aac aac ttt aat cag gag gct 213
 Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe Asn Gln Glu Ala
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gaa gac ctg tct tat caa agt tca ctt gct tct tgg aat tat aat act 261
 Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr
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aac att act gaa gaa aat gcc caa aag atg agt gag gct gca gcc aaa 309
 Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu Ala Ala Ala Lys
 55 60 65

tgg tct gcc ttt tat gaa gaa cag tct aag act gcc caa agt ttc tca 357
 Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala Gln Ser Phe Ser
 70 75 80

cta caa gaa atc cag act ccg atc atc aag cgt caa cta cag gcc ctt 405
 Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln Leu Gln Ala Leu
 85 90 95 100

cag caa agt ggg tct tca gca ctc tca gca gac aag aac aaa cag ttg 453
 Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys Asn Lys Gln Leu
 105 110 115

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 Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val
 120 125 130

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 Cys Asn Pro Arg Asn Pro Gln Glu Cys Leu Leu Leu Pro Gly Leu
 135 140 145

gat gaa ata atg gcg aca agc aca gac tac aac tct agg ctc tgg gca 597
 Asp Glu Ile Met Ala Thr Ser Thr Asp Tyr Asn Ser Arg Leu Trp Ala
 150 155 160

tgg gag ggc tgg agg gct gag gtt ggc aag cag ctg agg ccg ttg tat 645
 Trp Glu Gly Trp Arg Ala Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr
 165 170 175 180

gaa gag tat gtg gtc ctg aaa aac gag atg gca aga gca aac aat tat 693
 Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn Asn Tyr
 185 190 195

aac gac tat ggg gat tat tgg aga ggg gac tat gaa gca gag gga gca 741
 Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Ala Glu Gly Ala
 200 205 210

gat ggc tac aac tat aac cgt aac cag ttg att gaa gat gta gaa cgt 789

09978385-101601

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Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val	
230 235 240	
agg agg aag ttg atg gat acc tac cct tcc tac atc agc ccc act gga	885
Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile Ser Pro Thr Gly	
245 250 255 260	
tgc ctc cct gcc cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca	933
Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr	
265 270 275	
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Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys Pro Asn Ile Asp	
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Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala Glu Arg Ile Phe	
295 300 305	
caa gag gca gag aaa ttc ttt gtt tct gtt ggc ctt cct cat atg act	1077
Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu Pro His Met Thr	
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caa gga ttc tgg gca aac tct atg ctg act gag cca gca gat ggc cgg	1125
Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro Ala Asp Gly Arg	
325 330 335 340	
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Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly His Gly Asp Phe	
345 350 355	
aga atc aag atg tgt aca aag gtc aca atg gac aac ttc ttg aca gcc	1221
Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn Phe Leu Thr Ala	
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cat cac gag atg gga cac atc caa tat gac atg gca tat gcc agg caa	1269

09978385-101601

His His Glu Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Arg Gln	
375 380 385	
cct ttc ctg cta aga aac gga gcc aat gaa ggg ttc cat gaa gct gtt	1317
Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val	
390 395 400	
gga gaa atc atg tca ctt tct gca gct acc ccc aag cat ctg aaa tcc	1365
Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser	
405 410 415 420	
att ggt ctt ctg cca tcc gat ttt caa gaa gat agc gaa aca gag ata	1413
Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser Glu Thr Glu Ile	
425 430 435	
aac ttc cta ctg aaa cag gca ttg aca att gtt gga aca cta ccg ttt	1461
Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe	
440 445 450	
act tac atg tta gag aag tgg agg tgg atg gtc ttt cgg ggt gaa att	1509
Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe Arg Gly Glu Ile	
455 460 465	
ccc aaa gag cag tgg atg aaa aag tgg tgg gag atg aag cgg gag atc	1557
Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile	
470 475 480	
gtt ggt gtg gtg gag cct ctg cct cgt gat gaa aca tac tgt gac cct	1605
Val Gly Val Val Glu Pro Leu Pro Arg Asp Glu Thr Tyr Cys Asp Pro	
485 490 495 500	
gca tct ctg ttc cat gtt tct aat gat tac tca ttc att cga tat tac	1653
Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr	
505 510 515	
aca agg acc att tac caa ttc cag ttt caa gaa gct ctt tgt caa gca	1701
Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala	
520 525 530	
gct aag tat aat ggt tct ctg cac aaa tgt gac atc tca aat tcc act	1749

09978385.101601

Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile Ser Asn Ser Thr	
535 540 545	
gaa gct ggg cag aag ttg ctc aag atg ctg agt ctt gga aat tca gag	1797
Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu Gly Asn Ser Glu	
550 555 560	
ccc tgg acc gaa gcc ttg gaa aat gtg gta gga gca agg aat atg gat	1845
Pro Trp Thr Glu Ala Leu Glu Asn Val Val Gly Ala Arg Asn Met Asp	
565 570 575 580	
gta aaa cca ctg ctc aat tac ttc caa ccg ttg ttt gac tgg ctg aaa	1893
Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe Asp Trp Leu Lys	
585 590 595	
gag cag aac aga aat tct ttt gtg ggg tgg aac act gaa tgg agc cca	1941
Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr Glu Trp Ser Pro	
600 605 610	
tat gcc gac caa agc att aaa gtg agg ata agc cta aaa tca gct ctt	1989
Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu	
615 620 625	
gga gct aat gca tat gaa tgg acc aac aac gaa atg ttc ctg ttc cga	2037
Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met Phe Leu Phe Arg	
630 635 640	
tca tct gtt gca tat gcc atg aga aag tat tct tca ata atc aaa aac	2085
Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Ser Ser Ile Ile Lys Asn	
645 650 655 660	
cag aca gtt cct ttt cta gag gaa gat gta cga gtg agt gat ttg aaa	2133
Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val Ser Asp Leu Lys	
665 670 675	
cca aga gtc tcc ttc tac ttc ttt gtc acc tca ccc caa aat gtg tct	2181
Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro Gln Asn Val Ser	
680 685 690	
gat gtc att cct aga agt gaa gtt gaa gat gcc atc agg atg tct cgg	2229

00978385-101601

Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile Arg Met Ser Arg
 695 700 705

ggc cgc atc aat gat gtc ttt ggc ctg aat gat aac agc ctg gag ttt 2277
 Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn Ser Leu Glu Phe
 710 715 720

ctg ggg att cac cca aca ctt gag cca cct tac cag cct cct gtc acc 2325
 Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln Pro Pro Val Thr
 725 730 735 740

ata tgg ctg att att ttt ggt gtt gtg atg gca ctg gta gtg gtt ggc 2373
 Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu Val Val Val Gly
 745 750 755

atc atc atc ctg att gtc act ggg atc aaa ggt cga aag aag aaa aat 2421
 Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg Lys Lys Lys Asn
 760 765 770

gaa aca aaa aga gaa gag aac cct tat gac tcg atg gac att gga aaa 2469
 Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met Asp Ile Gly Lys
 775 780 785

gga gaa agc aat gca gga ttc caa aac agt gat gat gct cag act tcc 2517

Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp Ala Gln Thr Ser
 790 795 800

ttt tagcaaagca cttgtcatct tcctgtatgt aaatgctaac ttcatagtac 2570
 Phe
 805

acaaaatatg agagtataca catgtcatta gctatcaaaa ctatgatctg ttcagtaaac 2630
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09978385-101601

<400> 9

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			20					25					30		
Asn	Gln	Glu	Ala	Glu	Asp	Leu	Ser	Tyr	Gln	Ser	Ser	Leu	Ala	Ser	Trp
		35					40					45			
Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Ala	Gln	Lys	Met	Ser	Glu
	50					55					60				
Ala	Ala	Ala	Lys	Trp	Ser	Ala	Phe	Tyr	Glu	Glu	Gln	Ser	Lys	Thr	Ala
65					70					75					80
Gln	Ser	Phe	Ser	Leu	Gln	Glu	Ile	Gln	Thr	Pro	Ile	Ile	Lys	Arg	Gln
				85					90					95	
Leu	Gln	Ala	Leu	Gln	Gln	Ser	Gly	Ser	Ser	Ala	Leu	Ser	Ala	Asp	Lys
			100					105					110		
Asn	Lys	Gln	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser
		115					120					125			
Thr	Gly	Lys	Val	Cys	Asn	Pro	Arg	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu
	130					135					140				
Glu	Pro	Gly	Leu	Asp	Glu	Ile	Met	Ala	Thr	Ser	Thr	Asp	Tyr	Asn	Ser
145					150					155					160
Arg	Leu	Trp	Ala	Trp	Glu	Gly	Trp	Arg	Ala	Glu	Val	Gly	Lys	Gln	Leu
				165					170					175	
Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg
			180					185					190		
Ala	Asn	Asn	Tyr	Asn	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu
		195					200					205			
Ala	Glu	Gly	Ala	Asp	Gly	Tyr	Asn	Tyr	Asn	Arg	Asn	Gln	Leu	Ile	Glu
	210					215					220				
Asp	Val	Glu	Arg	Thr	Phe	Ala	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu
225					230					235					240
His	Ala	Tyr	Val	Arg	Arg	Lys	Leu	Met	Asp	Thr	Tyr	Pro	Ser	Tyr	Ile
				245					250					255	
Ser	Pro	Thr	Gly	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly
			260					265					270		
Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Pro	Leu	Thr	Val	Pro	Phe	Ala	Gln	Lys
			275				280					285			
Pro	Asn	Ile	Asp	Val	Thr	Asp	Ala	Met	Met	Asn	Gln	Gly	Trp	Asp	Ala
	290					295					300				
Glu	Arg	Ile	Phe	Gln	Glu	Ala	Glu	Lys	Phe	Phe	Val	Ser	Val	Gly	Leu
305					310					315					320

0978385.101601

Pro His Met Thr Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro
 325 330 335
 Ala Asp Gly Arg Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly
 340 345 350
 His Gly Asp Phe Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn
 355 360 365
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
 370 375 380
 Tyr Ala Arg Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
 385 390 395 400
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
 405 410 415
 His Leu Lys Ser Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser
 420 425 430
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
 435 440 445
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
 450 455 460
 Arg Gly Glu Ile Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met
 465 470 475 480
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Leu Pro Arg Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
 500 505 510
 Ile Arg Tyr Tyr Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala
 515 520 525
 Leu Cys Gln Ala Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile
 530 535 540
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu
 545 550 555 560
 Gly Asn Ser Glu Pro Trp Thr Glu Ala Leu Glu Asn Val Val Gly Ala
 565 570 575
 Arg Asn Met Asp Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe
 580 585 590
 Asp Trp Leu Lys Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr
 595 600 605
 Glu Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
 610 615 620
 Lys Ser Ala Leu Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met
 625 630 635 640
 Phe Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Ser Ser
 645 650 655

09070385.101601

Ile Ile Lys Asn Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val
 660 665 670
 Ser Asp Leu Lys Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro
 675 680 685
 Gln Asn Val Ser Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile
 690 695 700
 Arg Met Ser Arg Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn
 705 710 715 720
 Ser Leu Glu Phe Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln
 725 730 735
 Pro Pro Val Thr Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu
 740 745 750
 Val Val Val Gly Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg
 755 760 765
 Lys Lys Lys Asn Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met
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 Asp Ile Gly Lys Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp
 785 790 795 800
 Ala Gln Thr Ser Phe
 805

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 ggcagggagg catccagtgg

20

09978385.101601